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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/699,035	10/31/2003	John Francis Bateman	A36056-PCT-USA-A	3842

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EXAMINER	
HADDAD, MAHER M	
ART UNIT	**PAPER NUMBER**
1644	

DATE MAILED: 03/31/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/699,035	BATEMAN ET AL.	
	Examiner	Art Unit	
	Maher M. Haddad	1644	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 January 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,2,4,5,7,8,11 and 12* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-2, 4-5, 7-8 and 11-12* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☒ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Sequence alignment*.

DETAILED ACTION

1. Claims 1-2, 4-5, 7-8 and 11-12 are pending.

2. Applicant's election of Group I, claims 1-14 (now 1-2, 4-5, 7-8 and 11-12) drawn to an isolated polypeptide, derivative or homolog thereof of WARP and a polypeptide of human WARP of SEQ ID NO: 6 encoded by SEQ ID NO:5 and the VA domain of SEQ ID NO:2 encoded by SEQ ID NO: 1 as the species filed on 1/25/06, is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

3. Claims 1-2, 4-5, 7-8 and 11-12 are under examination as they read on an isolated polypeptide, derivative or homolog thereof of WARP and a polypeptide of human WARP of SEQ ID NO: 6 encoded by SEQ ID NO:5 and the VA domain of SEQ ID NO:2 encoded by SEQ ID NO: 1 as the species.

4. There does not appear to be a shared common structural relationship between the nucleotide of SEQ ID NO: 5 and the polypeptide of SEQ ID NO:6. SEQ ID NO:5 is missing a codon corresponding for Asp amino acid of SEQ ID NO: 6 at position 211.

5. The references cited in the Search Report PCT/AU02/00542 have been considered, but will not be listed on any patent resulting from this application because they were not provided on a separate list in compliance with 37 CFR 1.98(a)(1). In order to have the references printed on such resulting patent, a separate listing, preferably on a PTO/SB/08A and 08B form, must be filed within the set period for reply to this Office action.

6. Applicant's IDS, filed 10/4/04, is acknowledged, but will not be listed on any patent resulting from this application because they were not provided on a separate list in compliance with 37 CFR 1.98(a)(1). In order to have the references printed on such resulting patent, a separate listing, preferably on a PTO/SB/08A and 08B form, must be filed within the set period for reply to this Office action.

7. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Page 10, lines 2, 8, and 20, and page 53, ¶143 contain embedded hyperlinks and/or other forms of browser-executable code which are impermissible and require deletion.

8. The specification is objected to for the following informalities: The SUMMARY OF SEQUENCE IDENTIFIERS on pages 12-14, discloses several sequences, however, it is not

clear as what is the structural difference between SEQ ID NO: 6 and SEQ ID NO: 20. Further, in title of Example 11, the letter "f" should be "of". Correction is required.

9. The specification is objected to under 37 CFR 1.821(d) for failing to provide a sequence identifier for each individual sequence. Figure 1A, Figure 1C, Figure 2A, and Figure 2B on pages 9-10 have described several sequences that each must have a sequence identifier. Correction is required.

10. Acknowledgment is made of a claim for foreign priority under 35 U.S.C 119(a)-(d) for Australia PR4701, however no copies of the certified copies of the priority documents have been received in this National Stage application from the international Bureau. A courtesy copy is required.

11. Claims 7 and 11 are objected to because "a set forth" should be "as set forth". Correction is required.

12. The following is a quotation of the second paragraph of 35 U.S.C. 112.

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

13. Claims 1, 4, 7 and 11-12 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A. The recitation "substantially" in claims 1, 4, 7 and 11 are indefinite and ambiguous. The metes and bounds the term is not clear.

B. Claims 11-12 are indefinite. Claims 11-12 depend from claim 1, claim 1 recites a polypetide encoded by a nucleotide sequence having at least 65% similarity to SEQ ID NO:1, which is a fragment, however, claims 11-12 recite the fullength polypetide which fail to further limit the polypeptide.

14. 35 U.S.C. § 101 reads as follows:

"Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title".

15. Claims 1-2, 4-5, 7-8 and 11-12 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific and/or substantial asserted utility or a well established utility.

Applicant is directed to the Utility Examination Guidelines, Federal Register, Vol. 66, No. 4, pages 1092-1099, Friday January 5, 2001.

The instant application has provided a description of a nucleotide encoding a polypeptide and an antibody against the polypeptide. The instant application does not disclose the biological role of

the claimed polypeptide or its significance. The instant specification asserts specific utilities for the claimed invention as a molecular marker of the integrity of the extracellular matrix in an animal including a human subject. In particularly, the specification also asserts that thee polypeptide of the invention provides a molecular marker of cartilage integrity. Further, the specification asserts that the identification of the molecular marker in circulating or tissue fluid is indicative of disrepair of the extracellular matrix and in particular cartilage such as caused or facilitated by trauma or a degenerative disease or other condition , for example, arthritis or autoimmunity (see page 1, 1¶). In Addition the specification assets that the identification of the molecular marker of present invention enables the development of a range of diagnostic and therapeutic agents for degeneration of extracellular matrix or the poor development of the matrix at the fetal and postnatal stages, including testing for mutation in the gene sequence in human disease, such as, but not limited to, cartilage disease or arthritis (see page 2, 1¶). Furthermore, the specification on page 3, 4¶ discloses that the WARP protein is a member of the expanding von Willebrand factor Type A-domain (VA) protein superfamily participate in variety of functions including hemostasis, cell adhesion and protein-protein interactions between matrix molecules.

These utilities are not considered to be specific and substantial because the specification fails to disclose any particular function or biological significance for von Willebrand A-Related protein "WARP". The disclosed polypeptide is said to have a potential function based upon its amino acid sequence similarity (unspecified) to other known proteins comprising VA-domain such as FACIT collagen XII, XIV and the recently described FACIT collagen XX and XXI, the Matrilins and Cochlin. A-domains are thought to mediate interactions with other proteins via the metal ion dependant adhesion site (MIDAS) motif and their involvement in oligomerisation, filamentous network formation, and cell adhesion and spreading has been reported (see Example 11). After further research, specific and substantial credible utility might be found for the claimed isolated compositions. However, the specification on page 4, 5¶ discloses that the VA module is an independently folding protein unit that attains a classic αβ "Rossman" fold consisting of a parallel β sheet surrounded by amphipathic a helices, and in the majority of VA domains, a metal ion-dependent adhesion site (MIDAS) at the C-termianl end of the β sheet. This suggests that this domain originally evolved from a Rossmann fold acquiring specialized functions, apparently related to multiprotein assemblies and perhaps involving divalent cations.

This further characterization, however, is part of the act of invention and until it has been undertaken, Applicant's claimed invention is incomplete. While the specification on page 58 under Example 14 discloses that WARP is an oligomeric protein expressed in cartilage matrix, however, WARP also exists in a number of pools of differing solubilities and possibly different functions during development or maturation. However, since the specification fails to demonstrate "a differential expression" in both normal and a degenerative disease, methods of identifying or therapeutic regiments is not substantiated. The presence of WRAP in chondrocyte cells which is secreted to the cartilage matrix is not sufficient for establishing a utility in diagnosis of a disease in the absence of some information regarding a correlative or causal relationship between the expression of the polypeptide, and the disease. While a number of

diseases arise from mutations in VWA domains, the specification fails to identify any disease for comparative study, particularly those with WARP defects, to allow any in depth correlations to be derived.

The instant situation is directly analogous to that which was addressed in *Brenner V. Manson*, 148 U.S. P. Q. 689 (1966), in which a novel compound which was structurally analogous to other compounds which were known to possess anti-tumor activity was alleged to be potentially useful as an anti-tumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S. C. § 101, which requires that an invention must have either an immediately apparent or fully disclosed "real world" utility. The instant claims are drawn to a polypeptide of as yet undetermined function or biological significance. There is no evidence of record or any line of reasoning that would support a conclusion that the WARP of the instant application was, as of the filling date, involve in variety of functions including hemostasis, cell adhesion and protein-protein interactions between matrix molecules. Until some actual and specific significance can be attributed to the protein identified in the specification as WARP, one of ordinary skill in the art would be required to perform additional experimentation in order to determine how to use the claimed invention. Thus, there was no immediately apparent or "real world" utility as of the filing date.

No single effect of the disclosed WARP is ascribed to the claimed protein. Note that while the specification produces the full-length protein recombinantly, no biological activity is established for the full length protein or any of the claimed derivative or homolog thereof. As such, further research would be required to identify or research such as studying the properties of the claimed product itself or the mechanisms in which the material is involved would be required. Since the instant specification does not disclose a credible "real world" use for WARP, then the claimed invention as disclosed does not meet the requirements of 35 U.S. C. § 101 as being useful.

The proteins of the instant invention are compounds, which share some structural similarity with ECM proteins based on sequence similarity. It is not clear if the protein of the instant application would have the same function in variety of functions including hemostasis, cell adhesion and protein-protein interactions between matrix molecules. Attwood (Science 2000; 290:471-473) teaches that "[i]t is presumptuous to make functional assignments merely on the basis of some degree of similarity between sequences. Similarly, Skolnick et al. (Trends in Biotech. 2000; 18(1):34-39) teach that the skilled artisan is well aware that assigning functional activities for any particular protein or protein family based upon sequence homology is inaccurate, in part because of the multifunctional nature of proteins (e.g., "Abstract" and "Sequence-based approaches to function prediction", page 34). Even in situations where there is some confidence of a similar overall structure between two proteins, only experimental research can confirm the artisan's best guess as to the function of the structurally related protein (see in particular "Abstract" and Box 2). To employ the WARP protein of the instant invention in any of the disclosed methods would clearly be using it as the object of further research. Such a use has been determined by the courts to be a utility which, alone, does not support patentablility. Since the

instant specification does not disclose a "real world" use for "WARP", then the claimed invention as disclosed does not meet the requirement of 35 U.S.C. § 101 as being useful.

16. The following is a quotation of the first paragraph of 35 U.S.C. 112:
The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

17. Claims 1-2, 4-5, 7-8 and 11-12 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and/or substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to used the claimed invention.

Further, besides an isolated polypeptide comprising the polypeptide of human WARP of SEQ ID NO: 6, a polypeptide encoded by SEQ ID NO:5, an isolated polypeptide consisting of the VA domain of SEQ ID NO:2 encoded by SEQ ID NO: 1, the specification fails to provide any guidance as to how to make an isolated polypeptide or "any derivative or homolog thereof" which in situ forms part of the extracellular matrix (ECM) in a mammal, wherein said polypeptide "comprises" a von Willebrand Factor A (VA)-related domain encoded by a nucleotide sequence selected from the group consisting of: i) a nucleotide sequence substantially as set forth in SEQ ID NO: 1/5, ii) any nucleotide sequence "having" "at least about 65% similarity" to SEQ ID NO: 1/5; and iii) any nucleotide sequence "capable of hybridizing" to SEQ ID NO:1/5 or the complement of SEQ ID NO:1/5 under "low stringency conditions" in claims 1 and 4, wherein the nucleotide sequence is SEQ ID NO: 1/5 in claims 2 and 5, wherein the polypeptide comprising an amino acid sequence substantially as set forth in SEQ ID NO: 2, or an amino acid sequence having at least about 65% similarity to SEQ ID NO: 2/6 in claims 7/11, wherein the polpetide comprises the amino acid sequence set forth in SEQ ID NO: 2/6, in claims 8/12 . The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims.

There is insufficient guidance and direction as to how to make the claimed polypeptides or a derivative or homolog thereof, encoded by any nucleotide having at least about 65% similarity to SEQ ID NO:1/5 or capable of hybridizing to SEQ ID NO:1/5 or the complement of SEQ ID NO: 1/5 under low stringency conditions.

However, there does not appear to be sufficient guidance in the specification as filed as to how the skilled artisan would make and use the various amino acids recited in the instant claims. A person of skill in the art would not know which sequences are essential, which sequences are non-essential, and what particular sequence lengths identify essential sequences. There is insufficient guidance to direct a person of skill in the art to select particular sequences or sequence lengths as essential for use to the screening assay. Without detailed direction as to which nucleic acid sequences are essential to the function of the encoded polypeptide, a person

of skill in the art would not be able to determine without undue experimentation which of the plethora of nucleic acid sequences encompassed by the instant claims would share the ability as a molecular marker in circulatory or tissue fluid of degenerative disease, other than the nucleic acid of SEQ ID NO: 5 encoding the claimed polypeptide of SEQ ID NO:6. Further, the terms "comprising" and "having" are open-ended. They would open up the claimed molecule to include unspecified amino/nucleic acids on either or both terminal of the molecule.

The claims as written encompass a broad genus of protein with a large number of possibilities with regard to the length of the amino acid sequence. Further, making changes up to 35% of a cDNA sequence encoding the claimed protein does not provide that the encoded protein will retain the same function as the altered protein. Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are echoed by Doerks et al (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the databases, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity.

The fact that two nucleic acid sequences will hybridize under low stringent conditions does not in and of itself require that the two sequences share any functional activity. Thus the same observations apply to the recitation of "nucleotide sequence capable of hybridizing" under "low stringent hybridization conditions". Further, it was well known in the art at the time the invention was made that hybridization could occur between two sequence based upon short stretches of 100% identity. Thus a great deal of sequence variability *with respect to the full-length nucleic acid* is possible. In the absence of a clear recitation that the identity is over the full length of SEQ ID NO:1/5 the claim reads on subsequences. Finally, hybridization under conditions other than high stringency would be expected to permit a great deal of variation between the two hybridizing sequences, making it even more unpredictable that the two sequences would share the same function. Thus as for the recitation of percent identity and hybridization language in the absence of *a testable function* and limitations regarding both the *hybridization conditions* and the *sequence length over which the hybridization takes place*; does not allow the skilled artisan to make and use the hybridizing nucleic acids commensurate in scope with the instant claims without undue experimentation.

Further, with respect to derivative or homolog, the specification discloses (paragraphs 49 and 50), a "derivative" includes a mutant, fragment, part, portion or hybrid molecule. A derivative generally but not exclusively carries a single or multiple amino acid substitution, addition and/or deletion. A "homolog" includes an analogous polypeptide having at least about 65% similar amino acid sequence from another animal species or from a different locus within the same species. The claims are thus rendered so broad as to be essentially useless and although directed to a WARP polypeptide, is reminiscent of *Ex parte Maizel* (27 USPQ2d 1662 at 1665)

"Appellants have not chosen to claim the DNA by what it is but, rather, by what it does, i.e.,

encoding either a protein exhibiting certain characteristics, or a biologically functional equivalent thereof. Appellants' claims might be analogized to a single means claim of the type disparaged by the Court of Customs an Patent Appeals in *In re Hyatt*, 708F.2d 712, 218 USPQ 195 (Fed. Cir. 1983). The problem with the phrase "biologically functional equivalent thereof" is that it covers any conceivable means., i.e., cell or DNA, which achieves the stated biological result while the specification discloses, at most, only a specific DNA segment known to the inventor. Clearly the disclosure is not commensurate in scope with the claims."

Reasonable correlation must exist between the scope of the claims and scope of the enablement set forth. In view on the quantity of experimentation necessary the limited working examples, the nature of the invention, the state of the prior art, the unpredictability of the art and the breadth of the claims, it would take undue trials and errors to practice the claimed invention.

18. Claims 1-2, 4-5, 7-8 and 11-12 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant is in possession of an isolated polypeptide comprising the polypeptide of human WARP of SEQ ID NO: 6, a polypeptide encoded by SEQ ID NO:5, an isolated polypeptide consisting of the VA domain of SEQ ID NO:2 encoded by SEQ ID NO: 1.

Applicant is not in possession of an isolated polypeptide or "any derivative or homolog thereof" which in situ forms part of the extracellular matrix (ECM) in a mammal, wherein said polypeptide "comprises" a von Willebrand Factor A (VA)-related domain encoded by a nucleotide sequence selected from the group consisting of: i) a nucleotide sequence substantially as set forth in SEQ ID NO: 1/5, ii) any nucleotide sequence "having" "at least about 65% similarity" to SEQ ID NO: 1/5; and iii) any nucleotide sequence "capable of hybridizing" to SEQ ID NO:1/5 or the complement of SEQ ID NO:1/5 under "low stringency conditions" in claims 1 and 4, wherein the nucleotide sequence is SEQ ID NO: 1/5 in claims 2 and 5, wherein the polypeptide comprising an amino acid sequence substantially as set forth in SEQ ID NO: 2, or an amino acid sequence having at least about 65% similarity to SEQ ID NO: 2/6 in claims 7/11, wherein the polpetide comprises the amino acid sequence set forth in SEQ ID NO: 2/6, in claims 8/12.

Neither the exemplary embodiments nor the specification's general method appears to describe structural features, in structural terms, that are common to the genus. That is, the specification provides neither a representative number of species (WARP) to describe the claimed genus, nor does it provide a description of structural features that are common to species (WARP). The specification provides no structural description of WRAP other than ones specifically exemplified; in essence, the specification simply directs those skilled in the art to go figure out for themselves what the claimed derivatives and hamologs looks like. The specification's disclosure is inadequate to describe the claimed genus of WARP polypeptides.

Applicant has disclosed only amino/nucleic acid of SEQ ID NO: 1-8; therefore, the skilled artisan cannot envision all the contemplated polypeptide sequence possibilities recited in the instant claims. Consequently, conception cannot be achieved until a representative description of the structural and functional properties of the claimed invention has occurred, regardless of the complexity or simplicity of the method. Adequate written description requires more than a mere statement that it is part of the invention. See *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (CAFC1993). The Guidelines for the Examination of Patent Application Under the 35 U.S.C.112, ¶ 1"Written Description" Requirement make clear that the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species disclosure of relevant, identifying characteristics, i.e., structure or other physical and or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the genus (Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 20001, see especially page 1106 3rd column).

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.). Consequently, Applicant was not in possession of the instant claimed invention. See University of California v. Eli Lilly and Co. 43 USPQ2d 1398.

Applicant is directed to the final Guidelines for the Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001.

19. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless --

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e1) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

35 U.S.C. § 102(e), as revised by the AIPA and H.R. 2215, applies to all qualifying references, except when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. For such patents, the prior art date is determined under 35 U.S.C. § 102(e) as it existed prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. § 102(e)).

20. Claims 1-2, 4, 7-8 and 11 are rejected under 35 U.S.C. 102(b) as being anticipated by WO200118022 (provided by Application).

The `022 publication teaches a polypeptide encoded by a nucleotide sequence that is 100% identical to SEEQ ID NO: 1, said nucleotide sequence would hybridize to SEQ ID NO:1 or 5 under low stringency conditions (see attached sequence alignment in particular) as claimed in claims 1-2 and 4. The `022 publication also teaches a polypeptide encoded by a nucleotide sequence having at least 99% similarity to SEQ ID NO: 5, said nucleotide would hybridize to the complement of SEQ ID NO: 5 at low stringency condition (see attached sequence alignment in particular). Further the `022 publication teaches a 215 amino acids polypeptide comprising the amino acids sequence of SEQ ID NO: 2 (see claim 11 and attached sequence alignment in particular). Further the 215 amino acids polypeptide has 99.5% similarity to SEQ ID NO:6

The reference teachings anticipate the claimed invention.

21. Claims 1-2, 4, 7-8 and 11 are rejected under 35 U.S.C. 102(e) as being anticipated by US20060003323.

The `323 publication teaches a polypeptide encoded by a nucleotide sequence that is 100% identical to SEEQ ID NO: 1, said nucleotide sequence would hybridize to SEQ ID NO:1 or 5 under low stringency conditions (see published SEQ ID NO: 2 and attached sequence alignment in particular) as claimed in claims 1-2 and 4. The `323 publication also teaches a polypeptide encoded by a nucleotide sequence having at least 93% similarity to SEQ ID NO: 5, said nucleotide would hybridize to the complement of SEQ ID NO: 5 at low stringency condition (see attached sequence alignment in particular). Further the `323 publication teaches a 445 amino acids polypeptide comprising the amino acids sequence of SEQ ID NO: 2 (see attached sequence alignment in particular). Further the 445 amino acids polypeptide has 93% similarity to SEQ ID NO:6

The reference teachings anticipate the claimed invention.

22. No claim is allowed.

23. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maher Haddad whose telephone number is (571) 272-0845. The examiner can normally be reached Monday through Friday from 7:30 am to 4:00 pm. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on (571) 272-0841. The fax number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

March 15, 2006

Maher Haddad

Maher Haddad, Ph.D.
Patent Examiner
Technology Center 1600

XX
DR WPI; 2003-111873/10.
DR N-PSDB; AAD50397.
XX
PT New isolated Willebrand Factor A-Related Protein polypeptide useful for
PT the manufacture of a medicament in the treatment of a disease condition
PT of the extracellular matrix, in particular arthritis.
XX
PS Claim 7; Page 72-73; 103pp; English.
XX
CC The invention relates to Willebrand Factor A domain related-protein
CC (WARP) which is a member of von Willebrand Factor A (VA)-domain protein
CC superfamily of extracellular matrix (ECM) proteins. WARP is used as a
CC molecular marker, used for detecting a loss of ECM integrity in an animal
CC subject, monitoring repair, regeneration or other disease processes in an
CC animal subject and detecting a disease condition or a propensity for the
CC development of a disease condition in an animal subject. The invention is
CC useful for the manufacture of a medicament in the treatment of a disease
CC condition of the ECM. The disease condition involves the cartilage, and
CC is preferably arthritis. The invention is also used in gene therapy. The
CC present sequence is human VA domain
XX
SQ Sequence 180 AA;

Alignment Scores:

Pred. No.:	4.51e-69	Length:	180
Score:	902.00	Matches:	178
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	86.0%	Indels:	0
DB:	6	Gaps:	0

US-10-699-035A-1 (1-537) x AAE32500 (1-180)

```
Qy          1 GGGGACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GlyAspLeuMetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArg 21

Qy         61 GTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 ValArgGluPheValGlyGlnLeuValAlaProLeuProLeuGlyThrGlyAlaLeuArg 41

Qy        121 GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 AlaSerLeuValHisValGlySerArgProTyrThrGluProPheGlyGlnHisSer 61

Qy        181 TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 SerGlyGluAlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThrHis 81

Qy        241 ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 ThrGlyLeuAlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAlaArg 101

Qy        301 CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGly 121

Qy        361 CCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArg 141

Qy        421 GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPhe 161

Qy        481 GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTC 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 ValAspValAspAspLeuHisIleIleValGlnGluLeuArgGlySerIleLeu 179
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RESULT 2
AAB87344
ID AAB87344 standard; protein; 215 AA.

XX
AC AAB87344;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human gene 3 encoded secreted protein HNTEO78, SEQ ID NO:85.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerary; cell culture;
KW chemotaxis; food additive; binding partner identification.
XX
OS Homo sapiens.
XX
PN WO200118022-A1.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US024008.
XX
PR 03-SEP-1999; 99US-0152315P.
PR 03-SEP-1999; 99US-0152317P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;
PI Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW;
PI Moore PA, Shi Y, Wei Y, Florence KA;
XX
DR WPI; 2001-203081/20.
DR N-PSDB; AAF91860.
XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers.
XX
PS Claim 11; Page 532-533; 607pp; English.
XX
CC AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted
CC protein genes, and AAB87342-AAB87413 represent the proteins they encode.
CC AAB87414-AAB87454 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 52 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin
CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein of the invention

CC subject, monitoring repair, regeneration or other disease processes in an
CC animal subject and detecting a disease condition or a propensity for the
CC development of a disease condition in an animal subject. The invention is
CC useful for the manufacture of a medicament in the treatment of a disease
CC condition of the ECM. The disease condition involves the cartilage, and
CC is preferably arthritis. The invention is also used in gene therapy. The
CC present sequence is human VA domain
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 913; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-94;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 60

Qy         61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120

Qy        121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 180
```

RESULT 2
AAB87344
ID AAB87344 standard; protein; 215 AA.
XX
AC AAB87344;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human gene 3 encoded secreted protein HNTEO78, SEQ ID NO:85.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerary; cell culture;
KW chemotaxis; food additive; binding partner identification.
XX
OS Homo sapiens.
XX
PN WO200118022-A1.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US024008.
XX
PR 03-SEP-1999; 99US-0152315P.
PR 03-SEP-1999; 99US-0152317P.
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PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;
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PI Moore PA, Shi Y, Wei Y, Florence KA;
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DR WPI; 2001-203081/20.
DR N-PSDB; AAF91860.
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CC and their corresponding secreted proteins are useful for preventing,
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CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 52 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
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CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin
CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein of the invention
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 913; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2e-94;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 91

Qy         61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151

Qy        121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 211
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RESULT 3
ABG65347
ID ABG65347 standard; protein; 215 AA.
XX
AC ABG65347;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human albumin fusion protein #2022.
XX
KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177137-A1.

CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 299 AA;

WO 200118022 A1

Alignment Scores:

Pred. No.:	6.32e-86	Length:	299
Score:	1373.00	Matches:	282
Percent Similarity:	94.6%	Conservative:	0
Best Local Similarity:	94.6%	Mismatches:	8
Query Match:	57.7%	Indels:	8
DB:	3	Gaps:	3

US-10-699-035A-5 (1-1254) x AAB42581 (1-299)

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Qy          3 GCTCCCCTGGACGGCGCTCGGCCTGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGAGCGG 62
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Db          9 AlaProLeuAspGlyAlaArg-LeuAlaLeuSerLeuArg-TrpArgTrpArg------T 26

Qy         63 CGCGGAGCGCGGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGACAG 122
                        ||||||||||||||||||||      ||||||||||||||||||||||
Db         26 hrProAspCys--ProProAlaSerAlaProGlu---AspLeuMetPheLeuLeuAspSe 44

Qy        123 CTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCTGGT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         44 rSerAlaSerValSerHisTyrGluPheSerArgValArgGluPheValGlyGlnLeuVa 64

Qy        183 GGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCG 242
              ||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db         64 lAlaProLeuProLeuAlaPro***AlaLeuArgAlaSerLeuValHisValGlySerAr 84

Qy        243 GCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGATGCGGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 gProTyrThrGluProProPheGlyGlnHisSerSerGlyGluAlaAlaGlnAspAlaVa 104

Qy        303 GCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCGCTGGTCTATGCCAA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 lArgAlaSerAlaGlnArgMetGlyAspThrHisThrGlyLeuAlaLeuValTyrAlaLy 124

Qy        363 GGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTGTG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 sGluGlnLeuPheAlaGluAlaSerGlyAlaArgProGlyValProLysValLeuValTr 144

Qy        423 GGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCCATGCAGGAGCTCAAGGACCT 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 pValThrAspGlyGlySerSerAspProValGlyProProMetGlnGluLeuLysAspLe 164

Qy        483 GGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCCGC 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 uGlyValThrValPheIleValSerThrGlyArgGlyAsnPheLeuGluLeuSerAlaAl 184

Qy        543 TGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATCAT 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 aAlaSerAlaProAlaGluLysHisLeuHisPheValAspValAspAspLeuHisIleIl 204

Qy        603 TGTCCAAGAGCTGAGGGGCTCCATTCTC---GCGATGCGGCCGCAGCAGCTCCATGCCAC 659
              |||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db        204 eValGlnGluLeuArgGlySerIleLeuAspAlaMetArgProGlnGlnLeuHisAlaTh 224
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Qy        660 GGAGATCACGTCCAGCGGCTTCCGCCTGGCCTGGCCACCCCTGCTGACCGCAGACTCGGG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 rGluIleThrSerSerGlyPheArgLeuAlaTrpProProLeuLeuThrAlaAspSerGl 244

Qy        720 CTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGCCGGGGGCTGCAAGACGCCAGCAGCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 yTyrTyrValLeuGluLeuValProSerAlaGlnProGlyAlaAlaArgArgGlnGlnLe 264

Qy        780 GCCAGGGAACGCCACGGACTGGATCTGGGCCGGCCTCGACCCGGACACGGACTACGACGT 839
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Db        264 uProGlyAsnAlaThrAspTrpIleTrpAlaGlyLeuAspProAspThrAspTyrAspVa 284

Qy        840 GGCGCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATC 885
              |||||||||||||||||||||||||||||||||||||||||||||
Db        284 lAlaLeuValProGluSerAsnValArgLeuLeuArgProGlnIle 299
```

RESULT 9
AAB87344
ID AAB87344 standard; protein; 215 AA.
XX
AC AAB87344;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human gene 3 encoded secreted protein HNTEO78, SEQ ID NO:85.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
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KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerary; cell culture;
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XX
OS Homo sapiens.
XX
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DR N-PSDB; AAF91860.
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CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 52 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: February 13, 2006, 13:10:29 ; Search time 9.08696 Seconds
(without alignments)
603.637 Million cell updates/sec

Title: US-10-699-035A-6
Perfect score: 2154
Sequence: 1 MLPWTALGLALSLRLALARS.....RPRPRPVPRAPTPGTASREP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2130.5	98.9	445	6	US-10-453-372-2	Sequence 2, Appli
2	421.5	19.6	3063	7	US-11-186-284-26	Sequence 26, Appl
3	401	18.6	517	7	US-11-169-041-160	Sequence 160, App
4	253.5	11.8	915	6	US-10-131-826A-294	Sequence 294, App
5	253.5	11.8	956	7	US-11-113-424-39	Sequence 39, Appl
6	194	9.0	214	7	US-11-192-449-6	Sequence 6, Appli
7	194	9.0	214	7	US-11-192-449-9	Sequence 9, Appli
8	185	8.6	214	7	US-11-192-449-5	Sequence 5, Appli
9	184	8.5	678	6	US-10-063-703-34	Sequence 34, Appl
10	184	8.5	678	7	US-11-102-240-34	Sequence 34, Appl
11	175	8.1	709	6	US-10-453-372-186	Sequence 186, App
12	174	8.1	709	6	US-10-453-372-180	Sequence 180, App
13	174	8.1	1152	7	US-11-080-026-4	Sequence 4, Appli
14	173	8.0	709	6	US-10-453-372-182	Sequence 182, App
15	172.5	8.0	1167	6	US-10-601-368-18	Sequence 18, Appl
16	169	7.8	3570	6	US-10-453-372-178	Sequence 178, App
17	169	7.8	3570	6	US-10-453-372-196	Sequence 196, App
18	169	7.8	3570	6	US-10-453-372-198	Sequence 198, App
19	169	7.8	3570	6	US-10-453-372-200	Sequence 200, App
20	169	7.8	3570	6	US-10-453-372-202	Sequence 202, App
21	169	7.8	3570	6	US-10-453-372-204	Sequence 204, App
22	169	7.8	3570	6	US-10-453-372-206	Sequence 206, App
23	168	7.8	709	6	US-10-453-372-184	Sequence 184, App
24	168	7.8	3568	6	US-10-453-372-194	Sequence 194, App
25	162.5	7.5	847	6	US-10-995-561-634	Sequence 634, App
26	162.5	7.5	1259	6	US-10-995-561-625	Sequence 625, App
27	162.5	7.5	1286	6	US-10-995-561-628	Sequence 628, App
28	162.5	7.5	1341	6	US-10-995-561-621	Sequence 621, App
29	162.5	7.5	2217	7	US-11-193-561-38	Sequence 38, Appl
30	162.5	7.5	2217	7	US-11-193-771-38	Sequence 38, Appl
31	162.5	7.5	2217	7	US-11-193-789-38	Sequence 38, Appl
32	162.5	7.5	2217	7	US-11-193-806-38	Sequence 38, Appl
33	162.5	7.5	2217	7	US-11-193-857-38	Sequence 38, Appl
34	162.5	7.5	2330	7	US-11-193-561-21	Sequence 21, Appl
35	162.5	7.5	2330	7	US-11-193-771-21	Sequence 21, Appl
36	162.5	7.5	2330	7	US-11-193-789-21	Sequence 21, Appl
37	162.5	7.5	2330	7	US-11-193-806-21	Sequence 21, Appl
38	162.5	7.5	2330	7	US-11-193-857-21	Sequence 21, Appl
39	162.5	7.5	2355	6	US-10-995-561-623	Sequence 623, App
40	162.5	7.5	2355	6	US-10-995-561-627	Sequence 627, App
41	162.5	7.5	2355	7	US-11-193-561-19	Sequence 19, Appl
42	162.5	7.5	2355	7	US-11-193-771-19	Sequence 19, Appl
43	162.5	7.5	2355	7	US-11-193-789-19	Sequence 19, Appl
44	162.5	7.5	2355	7	US-11-193-806-19	Sequence 19, Appl
45	162.5	7.5	2355	7	US-11-193-857-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-453-372-2
; Sequence 2, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-2

Query Match 98.9%; Score 2130.5; DB 6; Length 445;
Best Local Similarity 93.9%; Pred. No. 3.9e-161;
Matches 418; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

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RESULT 2
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; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Query Match 19.6%; Score 421.5; DB 7; Length 3063;
Best Local Similarity 27.5%; Pred. No. 5.5e-25;
Matches 128; Conservative 59; Mismatches 174; Indels 105; Gaps 9;

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Qy        92 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151

Db       498 TKVEDIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAF 557

Qy       152 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI- 209

Db       558 RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVEDFDAFQRISFELTQSIC 617

Qy       210 ------LDAMR------PQQLHATEITSSGFRLAWPPL-------------LTADSGYYV 244

Db       618 LRIEQELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFSYHITYKEAAGDDEVTV 677

Qy       245 LE-------LVPSAQP-----------------------------GAARRQQLPGNATD 267

Db       678 VEPASSTSVVLSSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKVTDETTD 737

Qy       268 -----WIWA-----------------------------------GLDPDTDYDVALVPESN 288

Db       738 SFKITWTQAPGRVLRCRIIYRPVAGGESREVTTPPNQRRRTLENLIPDTKYEVSVIPEYF 797

Qy       289 VRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGE 348

Db       798 SGPGTPLTGNAATEEVRGNPRDLRVSDPTTSTMKLSWSGAPGKVKQ--YLVTYTPVAGGE 855

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RESULT 3
US-11-169-041-160
; Sequence 160, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-160

Query Match 18.6%; Score 401; DB 7; Length 517;
Best Local Similarity 30.0%; Pred. No. 2.2e-24;
Matches 114; Conservative 61; Mismatches 179; Indels 26; Gaps 6;

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Qy        36 MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE 95

Db       143 MFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKFTKVE 202

Qy        96 AAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPM 155

Db       203 DIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAFRDPA 262

Qy       156 QELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI----- 209

Db       263 IKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVEDFDAFQRISFELTQSICLRIE 322

Qy       210 --LDAMR------PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQL 261

Db       323 QELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFSYHI------TYKEAAGDDEV 376

Qy       262 ----PGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHAR 317

Db       377 TVVEPASSTSVVLNSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKVTDET 436
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: February 13, 2006, 13:10:29 ; Search time 3.91304 Seconds
(without alignments)
603.637 Million cell updates/sec

Title: US-10-699-035A-2
Perfect score: 913
Sequence: 1 RGDLMFLLDSSASVSHYEFS.....FVDVDDLHIIVQELRGSILD 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	913	100.0	445	6	US-10-453-372-2	Sequence 2, Appli
2	263.5	28.9	3063	7	US-11-186-284-26	Sequence 26, Appl
3	257.5	28.2	517	7	US-11-169-041-160	Sequence 160, App
4	251.5	27.5	915	6	US-10-131-826A-294	Sequence 294, App
5	251.5	27.5	956	7	US-11-113-424-39	Sequence 39, Appl
6	194	21.2	214	7	US-11-192-449-6	Sequence 6, Appli
7	194	21.2	214	7	US-11-192-449-9	Sequence 9, Appli
8	185	20.3	214	7	US-11-192-449-5	Sequence 5, Appli
9	183	20.0	678	6	US-10-063-703-34	Sequence 34, Appl
10	183	20.0	678	7	US-11-102-240-34	Sequence 34, Appl
11	163	17.9	709	6	US-10-453-372-186	Sequence 186, App
12	162.5	17.8	1152	7	US-11-080-026-4	Sequence 4, Appli
13	162	17.7	709	6	US-10-453-372-180	Sequence 180, App
14	162	17.7	3568	6	US-10-453-372-194	Sequence 194, App
15	162	17.7	3570	6	US-10-453-372-178	Sequence 178, App
16	162	17.7	3570	6	US-10-453-372-196	Sequence 196, App
17	162	17.7	3570	6	US-10-453-372-198	Sequence 198, App
18	162	17.7	3570	6	US-10-453-372-200	Sequence 200, App
19	162	17.7	3570	6	US-10-453-372-202	Sequence 202, App
20	162	17.7	3570	6	US-10-453-372-204	Sequence 204, App
21	162	17.7	3570	6	US-10-453-372-206	Sequence 206, App
22	161	17.6	709	6	US-10-453-372-182	Sequence 182, App
23	156	17.1	709	6	US-10-453-372-184	Sequence 184, App
24	150.5	16.5	1167	6	US-10-601-368-18	Sequence 18, Appl
25	149.5	16.4	182	6	US-10-601-368-25	Sequence 25, Appl
26	149.5	16.4	1141	6	US-10-601-368-24	Sequence 24, Appl
27	149.5	16.4	1166	6	US-10-601-368-22	Sequence 22, Appl
28	149.5	16.4	1188	6	US-10-601-368-21	Sequence 21, Appl
29	145.5	15.9	1147	6	US-10-453-372-4	Sequence 4, Appli
30	144.5	15.8	182	6	US-10-601-368-7	Sequence 7, Appli
31	144.5	15.8	1141	6	US-10-601-368-6	Sequence 6, Appli
32	144.5	15.8	1166	6	US-10-601-368-4	Sequence 4, Appli
33	144.5	15.8	1188	6	US-10-601-368-3	Sequence 3, Appli
34	144.5	15.8	1188	7	US-11-000-463-338	Sequence 338, App
35	144.5	15.8	1188	7	US-11-000-463-810	Sequence 810, App
36	144.5	15.8	2764	6	US-10-995-561-691	Sequence 691, App
37	144.5	15.8	2813	6	US-10-995-561-688	Sequence 688, App
38	144.5	15.8	2919	6	US-10-821-234-1133	Sequence 1133, Ap
39	133.5	14.6	1179	7	US-11-097-125-1	Sequence 1, Appli
40	133.5	14.6	1196	6	US-10-995-561-921	Sequence 921, App
41	133	14.6	184	6	US-10-665-658-7	Sequence 7, Appli
42	133	14.6	1170	7	US-11-080-026-2	Sequence 2, Appli
43	133	14.6	1170	7	US-11-107-028-4	Sequence 4, Appli
44	131	14.3	184	6	US-10-665-658-8	Sequence 8, Appli
45	128	14.0	1167	7	US-11-097-125-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-453-372-2
; Sequence 2, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH(
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-2

Query Match 100.0%; Score 913; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPPGQH 91

Qy         61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
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Db          92 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151

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Db         152 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 211
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RESULT 2
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Query Match 28.9%; Score 263.5; DB 7; Length 3063;
Best Local Similarity 35.8%; Pred. No. 1.1e-17;
Matches 64; Conservative 30; Mismatches 84; Indels 1; Gaps 1;

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Db         438 KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF 497

Qy          61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120

Db         498 TKVEDIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAF 557

Qy         121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178

Db         558 RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVEDFDAFQRISFELTQSI 616
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RESULT 3
US-11-169-041-160
; Sequence 160, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-160

Query Match 28.2%; Score 257.5; DB 7; Length 517;
Best Local Similarity 36.6%; Pred. No. 4.1e-18;
Matches 64; Conservative 27; Mismatches 83; Indels 1; Gaps 1;

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Qy          65 AAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPM 124

Db         203 DIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAFRDPA 262

Qy         125 QELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178

Db         263 IKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVEDFDAFQRISFELTQSI 317
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RESULT 4
US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588

GenCore version 5.1.7

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 13, 2006, 13:44:15 ; Search time 0.959464 Seconds
(without alignments)
1468.904 Million cell updates/sec

Title: US-10-699-035A-1
Perfect score: 1049
Sequence: 1 ggggacctgatgttcctgct.....tgaggggctccattctcgcg 537

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 194028

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/absS/ABSSWEB_spool/US10699035/runat_13022006_062453_25634/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10699035_@CGN_1_1_10_@runat_13022006_062453_25634 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	902	86.0	445	6	US-10-453-372-2	Sequence 2, Appli
2	261.5	24.9	3063	7	US-11-186-284-26	Sequence 26, Appl
3	257.5	24.5	517	7	US-11-169-041-160	Sequence 160, App
4	246.5	23.5	915	6	US-10-131-826A-294	Sequence 294, App
5	246.5	23.5	956	7	US-11-113-424-39	Sequence 39, Appl
6	197	18.8	214	7	US-11-192-449-6	Sequence 6, Appli
7	197	18.8	214	7	US-11-192-449-9	Sequence 9, Appli
8	188	17.9	214	7	US-11-192-449-5	Sequence 5, Appli
9	183	17.4	678	6	US-10-063-703-34	Sequence 34, Appl
10	183	17.4	678	7	US-11-102-240-34	Sequence 34, Appl
11	166.5	15.9	1152	7	US-11-080-026-4	Sequence 4, Appli
12	162	15.4	709	6	US-10-453-372-186	Sequence 186, App
13	161	15.3	709	6	US-10-453-372-180	Sequence 180, App
14	161	15.3	3568	6	US-10-453-372-194	Sequence 194, App
15	161	15.3	3570	6	US-10-453-372-178	Sequence 178, App
16	161	15.3	3570	6	US-10-453-372-196	Sequence 196, App
17	161	15.3	3570	6	US-10-453-372-198	Sequence 198, App
18	161	15.3	3570	6	US-10-453-372-200	Sequence 200, App
19	161	15.3	3570	6	US-10-453-372-202	Sequence 202, App
20	161	15.3	3570	6	US-10-453-372-204	Sequence 204, App
21	161	15.3	3570	6	US-10-453-372-206	Sequence 206, App
22	160	15.3	709	6	US-10-453-372-182	Sequence 182, App
23	155	14.8	709	6	US-10-453-372-184	Sequence 184, App
24	150.5	14.3	1167	6	US-10-601-368-18	Sequence 18, Appl
25	150	14.3	1141	6	US-10-601-368-24	Sequence 24, Appl
26	150	14.3	1166	6	US-10-601-368-22	Sequence 22, Appl
27	150	14.3	1188	6	US-10-601-368-21	Sequence 21, Appl
28	149.5	14.3	182	6	US-10-601-368-25	Sequence 25, Appl
29	145.5	13.9	1147	6	US-10-453-372-4	Sequence 4, Appli
30	145	13.8	1141	6	US-10-601-368-6	Sequence 6, Appli
31	145	13.8	1166	6	US-10-601-368-4	Sequence 4, Appli
32	145	13.8	1188	6	US-10-601-368-3	Sequence 3, Appli
33	145	13.8	1188	7	US-11-000-463-338	Sequence 338, App
34	145	13.8	1188	7	US-11-000-463-810	Sequence 810, App
35	144.5	13.8	182	6	US-10-601-368-7	Sequence 7, Appli
36	144.5	13.8	2764	6	US-10-995-561-691	Sequence 691, App
37	144.5	13.8	2813	6	US-10-995-561-688	Sequence 688, App
38	144.5	13.8	2919	6	US-10-821-234-1133	Sequence 1133, Ap
39	134.5	12.8	1179	7	US-11-097-125-1	Sequence 1, Appli
40	134.5	12.8	1196	6	US-10-995-561-921	Sequence 921, App
41	134	12.8	184	6	US-10-665-658-8	Sequence 8, Appli
42	133	12.7	184	6	US-10-665-658-7	Sequence 7, Appli
43	133	12.7	1170	7	US-11-080-026-2	Sequence 2, Appli
44	133	12.7	1170	7	US-11-107-028-4	Sequence 4, Appli
45	128	12.2	1167	7	US-11-097-125-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-453-372-2
; Sequence 2, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METI
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 2
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
-10-453-372-2

ignment Scores:

ed. No.:	1.63e-62	Length:	445
ore:	902.00	Matches:	178
rcent Similarity:	100.0%	Conservative:	0
st Local Similarity:	100.0%	Mismatches:	0
ery Match:	86.0%	Indels:	0
:	6	Gaps:	0

-10-699-035A-1 (1-537) x US-10-453-372-2 (1-445)

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Y          1 GGGGACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGG 60
b         33 GlyAspLeuMetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArg 52

y         61 GTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGT 120
b         53 ValArgGluPheValGlyGlnLeuValAlaProLeuProLeuGlyThrGlyAlaLeuArg 72

y        121 GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC 180
b         73 AlaSerLeuValHisValGlySerArgProTyrThrGluPheProPheGlyGlnHisSer 92

y        181 TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC 240
b         93 SerGlyGluAlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThrHis 112

Qy       241 ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG 300
Db       113 ThrGlyLeuAlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAlaArg 132

Qy       301 CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC 360
Db       133 ProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGly 152

Qy       361 CCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA 420
Db       153 ProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArg 172

Qy       421 GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTT 480
Db       173 GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPhe 192

Qy       481 GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTC 534
Db       193 ValAspValAspAspLeuHisIleIleValGlnGluLeuArgGlySerIleLeu 210
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RESULT 2
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Alignment Scores:

Pred. No.:	2.2e-13	Length:	3063
Score:	261.50	Matches:	64
Percent Similarity:	52.5%	Conservative:	29
Best Local Similarity:	36.2%	Mismatches:	83
Query Match:	24.9%	Indels:	1
DB:	7	Gaps:	1

US-10-699-035A-1 (1-537) x US-11-186-284-26 (1-3063)

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Qy         4 GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT 63
Db       440 AspIleValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheValLysVal 459

Qy        64 CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC 123
Db       460 ArgAlaPheLeuGluValLeuValLysSerPheGluIleSerProAsnArgValGlnIle 479

Qy       124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG 183
Db       480 SerLeuValGlnTyrSerArgAspProHisThrGluPheThrLeuLysLysPheThrLys 499

Qy       184 GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACT 243
Db       500 ValGluAspIleIleGluAlaIleAsnThrPheProTyrArgGlyGlySerThrAsnThr 519

Qy       244 GGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCA 303
Db       520 GlyLysAlaMetThrTyrValArgGluLysIlePheValProSerLysGlySerArgSer 539

Qy       304 GGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCC 363
Db       540 AsnValProLysValMetIleLeuIleThrAspGlyLysSerSerAspAlaPheArgAsp 559

Qy       364 CCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGC 423
Db       560 ProAlaIleLysLeuArgAsnSerAspValGluIlePheAlaValGlyValLysAspAla 579

Qy       424 AACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTG 483
Db       580 ValArgSerGluLeuGluAlaIleAlaSerProProAlaGluThrHisValPheThrVal 599

Qy       484 ---GACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATT 531
Db       600 GluAspPheAspAlaPheGlnArgIleSerPheGluLeuThrGlnSerIle 616
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RESULT 3
US-11-169-041-160
; Sequence 160, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28

GenCore version 5.1.7

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 13, 2006, 13:44:15 ; Search time 2.24054 Seconds
(without alignments)
1468.904 Million cell updates/sec

Title: US-10-699-035A-5
Perfect score: 2380
Sequence: 1 atgctcccctggacggcgct.....ccgccagccgtgagccgtaa 1254

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 194028

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10699035/runat_13022006_062453_25634/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10699035_@CGN_1_1_10_@runat_13022006_062453_25634 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2114	88.8	445	6	US-10-453-372-2	Sequence 2, Appli
	2	419	17.6	3063	7	US-11-186-284-26	Sequence 26, Appl
	3	398.5	16.7	517	7	US-11-169-041-160	Sequence 160, App
c	4	254.5	10.7	1717	7	US-11-182-016-20	Sequence 20, Appl
	5	253.5	10.7	915	6	US-10-131-826A-294	Sequence 294, App
	6	253.5	10.7	956	7	US-11-113-424-39	Sequence 39, Appl
	7	221.5	9.3	1366	6	US-10-821-234-1431	Sequence 1431, Ap
	8	221.5	9.3	1366	7	US-11-186-284-31	Sequence 31, Appl
	9	215	9.0	1496	7	US-11-186-284-35	Sequence 35, Appl
	10	212	8.9	1464	7	US-11-000-463-243	Sequence 243, App
	11	212	8.9	1464	7	US-11-186-284-28	Sequence 28, Appl
	12	212	8.9	1464	7	US-11-021-603-2	Sequence 2, Appli
	13	212	8.9	1467	6	US-10-821-234-1096	Sequence 1096, Ap
c	14	211	8.9	1464	7	US-11-000-463-243	Sequence 243, App
c	15	211	8.9	1464	7	US-11-186-284-28	Sequence 28, Appl
c	16	211	8.9	1464	7	US-11-021-603-2	Sequence 2, Appli
c	17	211	8.9	1467	6	US-10-821-234-1096	Sequence 1096, Ap
	18	210.5	8.8	1166	6	US-10-821-234-964	Sequence 964, App
	19	210.5	8.8	1466	7	US-11-186-284-33	Sequence 33, Appl
c	20	206.5	8.7	1733	7	US-11-182-016-21	Sequence 21, Appl
c	21	203.5	8.6	1466	7	US-11-186-284-33	Sequence 33, Appl
	22	202	8.5	1733	7	US-11-182-016-21	Sequence 21, Appl
c	23	200.5	8.4	1823	6	US-10-995-561-988	Sequence 988, App
c	24	200.5	8.4	2102	6	US-10-995-561-990	Sequence 990, App
c	25	200.5	8.4	2108	6	US-10-995-561-989	Sequence 989, App
c	26	200.5	8.4	2157	6	US-10-995-561-991	Sequence 991, App
	27	199	8.4	214	7	US-11-192-449-6	Sequence 6, Appli
	28	199	8.4	214	7	US-11-192-449-9	Sequence 9, Appli
	29	199	8.4	1717	7	US-11-182-016-20	Sequence 20, Appl
c	30	198.5	8.3	1366	6	US-10-821-234-1431	Sequence 1431, Ap
c	31	198.5	8.3	1366	7	US-11-186-284-31	Sequence 31, Appl
c	32	198.5	8.3	1742	7	US-11-182-016-23	Sequence 23, Appl
c	33	197	8.3	843	7	US-11-129-104-89	Sequence 89, Appl
	34	196.5	8.3	3570	6	US-10-453-372-196	Sequence 196, App
	35	195.5	8.2	3570	6	US-10-453-372-178	Sequence 178, App
	36	195.5	8.2	3570	6	US-10-453-372-198	Sequence 198, App
	37	195.5	8.2	3570	6	US-10-453-372-200	Sequence 200, App
	38	195.5	8.2	3570	6	US-10-453-372-202	Sequence 202, App
	39	195.5	8.2	3570	6	US-10-453-372-204	Sequence 204, App
	40	195.5	8.2	3570	6	US-10-453-372-206	Sequence 206, App
	41	192.5	8.1	1251	7	US-11-149-003-16	Sequence 16, Appl
	42	192	8.1	709	6	US-10-453-372-182	Sequence 182, App
c	43	191	8.0	495	7	US-11-182-016-31	Sequence 31, Appl
	44	190.5	8.0	709	6	US-10-453-372-180	Sequence 180, App
	45	190.5	8.0	709	6	US-10-453-372-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-10-453-372-2
; Sequence 2; Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH(
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-2

Alignment Scores:

Pred. No.:	2.77e-113	Length:	445
Score:	2114.00	Matches:	417
Percent Similarity:	93.7%	Conservative:	0
Best Local Similarity:	93.7%	Mismatches:	0
Query Match:	88.8%	Indels:	28
DB:	6	Gaps:	2

US-10-699-035A-5 (1-1254) x US-10-453-372-2 (1-445)

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Qy          1 ATGCTCCCCTGGACGGCGCTCGGCCTGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGAGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLeuProTrpThrAlaLeuGlyLeuAlaLeuSerLeuArgLeuAlaLeuAlaArgSer 20

Qy         61 GGCGCGGAGCGCGGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GlyAlaGluArgGlyProProAlaSerAlaProArgGlyAspLeuMetPheLeuLeuAsp 40

Qy        121 AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 SerSerAlaSerValSerHisTyrGluPheSerArgValArgGluPheValGlyGlnLeu 60

Qy        181 GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ValAlaProLeuProLeuGlyThrGlyAlaLeuArgAlaSerLeuValHisValGlySer 80

Qy        241 CGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGATGCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ArgProTyrThrGluPheProPheGlyGlnHisSerSerGlyGluAlaAlaGlnAspAla 100

Qy        301 GTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCGCTGGTCTATGCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ValArgAlaSerAlaGlnArgMetGlyAspThrHisThrGlyLeuAlaLeuValTyrAla 120

Qy        361 AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LysGluGlnLeuPheAlaGluAlaSerGlyAlaArgProGlyValProLysValLeuVal 140

Qy        421 TGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCCATGCAGGAGCTCAAGGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TrpValThrAspGlyGlySerSerAspProValGlyProProMetGlnGluLeuLysAsp 160

Qy        481 CTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LeuGlyValThrValPheIleValSerThrGlyArgGlyAsnPheLeuGluLeuSerAla 180

Qy        541 GCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AlaAlaSerAlaProAlaGluLysHisLeuHisPheValAspValAspAspLeuHisIle 200

Qy        601 ATTGTCCAAGAGCTGAGGGGCTCCATTCTC---GCGATGCGGCCGCAGCAGCTCCATGCC 657
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        201 IleValGlnGluLeuArgGlySerIleLeuAspAlaMetArgProGlnGlnLeuHisAla 220

Qy        658 ACGGAGATCACGTCCAGCGGCTTCCGCCTGGCCTGGCCACCCCTGCTGACCGCAGACTCG 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ThrGluIleThrSerSerGlyPheArgLeuAlaTrpProProLeuLeuThrAlaAspSer 240

Qy        718 GGCTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGCCGGGGGCTGCAAGACGCCAGCAG 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GlyTyrTyrValLeuGluLeuValProSerAlaGlnProGlyAlaAlaArgArgGlnGln 260

Qy        778 CTGCCAGGGAACGCCACGGACTGGATCTGGGCCGGCCTCGACCCGGACACGGACTACGAC 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 LeuProGlyAsnAlaThrAspTrpIleTrpAlaGlyLeuAspProAspThrAspTyrAsp 280

Qy        838 GTGGCGCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTGCGGGTGCGC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 ValAlaLeuValProGluSerAsnValArgLeuLeuArgProGlnIleLeuArgValArg 300

Qy        898 ACGCGG---------------------------------------------------- 903
              ||||||
Db        301 ThrArgProGlyGluAlaGlyProGlyAlaSerGlyProGluSerGlyAlaGlyProAla 320

Qy        904 --------------------------CCAGAGGAGGCCGGGCCAGAGCGCATCGTCATC 936
                                       ||||||||||||||||||||||||||||||||||
Db        321 ProThrGlnLeuAlaAlaLeuProAlaProGluGluAlaGlyProGluArgIleValIle 340

Qy        937 TCCCACGCCCGGCCGCGCAGCCTCCGCGTGAGTTGGGCCCCAGCGCTGGGCTCAGCCGCG 996
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 SerHisAlaArgProArgSerLeuArgValSerTrpAlaProAlaLeuGlySerAlaAla 360

Qy        997 GCGCTCGGCTACCACGTGCAGTTCGGGCCGCTGCGGGGCGGGGAGGCGCAGCGGGTGGAG 1056
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AlaLeuGlyTyrHisValGlnPheGlyProLeuArgGlyGlyGluAlaGlnArgValGlu 380

Qy       1057 GTGCCCGCGGGCCGCAACTGCACCACGCTGCAGGGCCTGGCGCCGGGCACCGCCTACCTG 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ValProAlaGlyArgAsnCysThrThrLeuGlnGlyLeuAlaProGlyThrAlaTyrLeu 400

Qy       1117 GTGACCGTGACCGCCGCCTTCCGCTCGGGCCGCGAGAGCGCGCTGTCCGCCAAGGCCTGC 1176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ValThrValThrAlaAlaPheArgSerGlyArgGluSerAlaLeuSerAlaLysAlaCys 420

Qy       1177 ACGCCCGACGGCCCCGCGCCCGCGCCCACGCCCCGTGCCCCGCGCCCCGACCCCGGGGACC 1236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ThrProAspGlyProArgProArgProArgProValProArgAlaProThrProGlyThr 440

Qy       1237 GCCAGCCGTGAGCCG 1251
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Db        441 AlaSerArgGluPro 445
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RESULT 2
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Alignment Scores:

Pred. No.:	1.5e-17	Length:	3063
Score:	419.00	Matches:	128